GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: October 28, 2000, 18:46:59 ; Search time 970.13 Seconds
(without alignments)
1796.320 Million cell updates/sec

Title: US-09-157-984-2
Perfect score: 399
Sequence: 1 aaggccaacgacttcttgca.....gccgcaactcatggaggcat 399

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pr1:*
10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sy:*
14: gb_un:*
15: em_fun:*
16: em_hum1:*
17: em_hum2:*
18: em_in:*
19: em_om:*
20: em_or:*
21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vi:*
30: gb_htg1:*
31: gb_htg2:*
32: gb_in1:*
33: gb_in2:*
34: em_ba1:*
35: em_ba2:*
36: em_hum3:*
37: em_hum4:*
38: gb_pr4:*
39: gb_htg3:*
40: gb_htg4:*
41: gb_htg5:*
42: gb_htg6:*
43: gb_htg7:*
44: em_htg1:*
45: em_htg2:*
46: em_htg3:*
47: em_hum5:*
48: gb_pl3:*
49: gb_pr5:*
50: gb_htg8:*
51: gb_htg9:*
52: gb_htg10:*
53: gb_htg11:*
54: gb_htg12:*
55: gb_htg13:*
56: gb_htg14:*
57: gb_in3:*
58: gb_htg15:*
59: gb_htg16:*
60: gb_htg17:*
61: em_htg4:*
62: em_htg5:*
63: em_htg6:*
64: em_htg7:*
65: em_hum6:*
66: gb_htg18:*
67: gb_htg19:*
68: gb_htg20:*
69: gb_htg21:*
70: gb_htg22:*
71: gb_htg23:*
72: gb_vi1:*
73: gb_vi2:*
74: gb_ba3:*
75: em_htg8:*
76: em_htg9:*
77: em_htg10:*
78: em_htg11:*
79: em_htg12:*
80: em_htg13:*
81: em_htg14:*
82: em_htg15:*
83: em_htg16:*
84: em_htg17:*
85: em_htg18:*
86: em_htg19:*
87: em_htg20:*
88: em_htg21:*
89: em_htg22:*
90: em_htg23:*
91: gb_pr6:*
92: gb_pr7:*
93: gb_sts1:*
94: gb_sts2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	399	100.0	519	4	CCU94949	U94949 Cyprinus ca
2	328.6	82.4	1218	4	AF055906	AF055906 Danio rer
3	129.2	32.4	1429	4	XIPNE6G	L36326 Xiphophorus
4	129.2	32.4	1429	4	XIPNE6R	L36325 Xiphophorus
5	129.2	32.4	1429	5	A46744	A46744 Sequence 1
6	127.6	32.0	1700	4	XIPNRTN6A	L36942 Xiphpophoru
7	127.6	32.0	2273	5	A46746	A46746 Sequence 3
8	123.6	31.0	720	4	XMNGFAA	X59941 X.maculatus
9	103.8	26.0	763	3	PIGNGFB	L31898 Pig nerve g
10	99.6	25.0	1123	12	MUSGFN4	M17298 Mouse nerve
11	99.6	25.0	1176	12	MMNGF1	V00836 Mouse mRNA
12	99.6	25.0	1176	12	MUSNGF	M35075 Mouse nerve

13	98	24.6	378	3	BOVNGFA	M26809 Bovine nerv
14	98	24.6	1164	12	MUSNGFB	K01759 Mouse beta-
15	98	24.6	1164	12	MUSNGFBA	M14805 Mouse nerve
16	96.4	24.2	1682	12	RATNGFB	M36589 Rat beta-ne
17	94.2	23.6	769	9	AB037520	AB037520 Pongo pyg
18	93.2	23.4	694	3	BTNGFB	Y09566 B.taurus ge
19	93.2	23.4	1169	12	PYXNGFSEQ	M22748 Praomys nat
20	92.4	23.2	1038	12	S62089	S62089 Mus sp. ner
21	89.4	22.4	725	5	I36342	I36342 Sequence 2
22	89.4	22.4	726	11	AF150960	AF150960 Homo sapi
23	89.4	22.4	769	9	AB037517	AB037517 Homo sapi
24	89.4	22.4	769	9	AB037518	AB037518 Pan trogl
25	89.4	22.4	972	5	E02939	E02939 DNA sequenc
26	89.4	22.4	972	5	E02982	E02982 DNA encodin
27	89.4	22.4	972	5	E03015	E03015 DNA encodin
28	89.4	22.4	972	5	E03037	E03037 DNA encodin
29	89.4	22.4	972	5	E03589	E03589 DNA encodin
30	89.4	22.4	972	5	E05802	E05802 Human NGF g
31	89.4	22.4	972	5	E08424	E08424 Genomic DNA
32	89.4	22.4	1047	91	HSBNGFAC	X52599 Human mRNA
33	89.4	22.4	4044	5	E00327	E00327 DNA coding
34	89.4	22.4	5778	92	HUMNGFBA2	M21062 Human nerve
35	89.4	22.4	11594	91	HSBNGF	V01511 H.sapiens g
36	89.4	22.4	116520	91	HSJ662B22	AL049825 Human DNA
37	87.8	22.0	769	9	AB037519	AB037519 Gorilla g
38	87.4	21.9	389	5	I36343	I36343 Sequence 5
39	86	21.6	372	4	CHKNGFC	M26810 Chicken ner
40	86	21.6	542	4	CHKNGFBA	D00010 Gallus gall
41	86	21.6	542	4	GGNGFB	X04067 Chicken bet
42	85.2	21.4	394	5	A68467	A68467 Sequence 4
43	84.6	21.2	354	92	S76884	S76884 Homo sapien
44	84.6	21.2	388	5	E02940	E02940 Synthetic D
45	84.4	21.2	1156	4	GGNGFB3E	X04003 Chicken bet

ALIGNMENTS

```
RESULT   1
CCU94949
LOCUS       CCU94949      519 bp    DNA             VRT       06-JUL-1998
DEFINITION  Cyprinus carpio NGF/NT-6-like neurotrophin (NNT) gene, partial cds.
ACCESSION   U94949
VERSION     U94949.1  GI:3290009
KEYWORDS    .
SOURCE      common carp.
  ORGANISM  Cyprinus carpio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
REFERENCE   1  (bases 1 to 519)
  AUTHORS   Lai,K.O., Fu,W.Y., Ip,F.C. and Ip,N.Y.
  TITLE     Cloning and expression of a novel neurotrophin, NT-7, from carp
  JOURNAL   Mol. Cell. Neurosci. 11 (1-2), 64-76 (1998)
  MEDLINE   98271461
REFERENCE   2  (bases 1 to 519)
  AUTHORS   Lai,K.O., Fu,W.Y., Ip,C.F. and Ip,N.Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAR-1997) Biology, The Hong Kong University of
            Science and Technology, Clear Water Bay, Kowloon, Hong Kong
FEATURES             Location/Qualifiers
     source          1. .519
                     /organism="Cyprinus carpio"
                     /db_xref="taxon:7962"
     gene            <1. .423
                     /gene="NNT"
     CDS             <1. .423
                     /gene="NNT"
                     /codon_start=1
                     /product="NGF/NT-6-like neurotrophin"
                     /protein_id="AAC25632.1"
                     /db_xref="GI:3290010"
                     /translation="PGPRVRRKANDFLHRGEYSVCDSEEHWVGNLTQATDLRGNEVTV
                     LPHVRINNVVKKQMFYETTCRVSKPIGAPKPGQGVSGVKAGTSSCRGIDNEHWNSYCT
                     NVHTFVRALTSYKNQIAWRFIRINAACVCVLSRNSWRH"
BASE COUNT      125 a    155 c    138 g    101 t
ORIGIN
```

```
  Query Match          100.0%;  Score 399;  DB 4;  Length 519;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-93;
  Matches  399;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 aaggccaacgacttcttgcatcgcggcgagtactctgtgtgtgacagcgaagagcactgg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 AAGGCCAACGACTTCTTGCATCGCGGCGAGTACTCTGTGTGTGACAGCGAAGAGCACTGG 81

Qy      61 gttggcaacctgacccaagccacagacttacggggcaatgaagtcacggtgctgccacat 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 GTTGGCAACCTGACCCAAGCCACAGACTTACGGGGCAATGAAGTCACGGTGCTGCCACAT 141

Qy     121 gttcgcatcaacaacgtggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcg 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     142 GTTCGCATCAACAACGTGGTGAAGAAGCAGATGTTCTACGAGACCACGTGCCGTGTGTCG 201

Qy     181 aagcccatcggggcccccaagccgggtcaaggagtcagcggcgttaaagcaggaacctct 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     202 AAGCCCATCGGGGCCCCCAAGCCGGGTCAAGGAGTCAGCGGCGTTAAAGCAGGAACCTCT 261

Qy     241 agctgtcgtgggatcgacaacgagcactggaactcttattgcaccaacgtgcacacctttt 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     262 AGCTGTCGTGGGATCGACAACGAGCACTGGAACTCTTATTGCACCAACGTGCACACCTTT 321

Qy     301 gtgcgggcgttaacgtcctacaaaaaccagattgcctggaggttcatccgaatcaacgcc 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     322 GTGCGGGCGTTAACGTCCTACAAAAACCAGATTGCCTGGAGGTTCATCCGAATCAACGCC 381

Qy     361 gcttgcgtgtgcgtcctcagccgcaactcatggaggcat 399
           |||||||||||||||||||||||||||||||||||||||
Db     382 GCTTGCGTGTGCGTCCTCAGCCGCAACTCATGGAGGCAT 420
```

```
RESULT   2
AF055906
LOCUS       AF055906     1218 bp    DNA             VRT       13-APR-1998
DEFINITION  Danio rerio neurotrophin-7 gene, complete cds.
ACCESSION   AF055906
VERSION     AF055906.1  GI:3044090
KEYWORDS    .
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Rasborinae; Danio.
REFERENCE   1  (bases 1 to 1218)
  AUTHORS   Nilsson,A.S., Fainzilber,M., Falck,P. and Ibanez,C.F.
  TITLE     Neurotrophin-7: a novel member of the neurotrophin family from the
            zebrafish
  JOURNAL   FEBS Lett. 424 (3), 285-290 (1998)
  MEDLINE   98198571
REFERENCE   2  (bases 1 to 1218)
  AUTHORS   Nilsson,A.-S., Fainzilber,M., Falck,P. and Ibanez,C.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-1998) Neuroscience, Karolinska Institute,
            Doktorsringen 12, Stockholm 17177, Sweden
FEATURES             Location/Qualifiers
     source          1. .1218
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
     mRNA            <348. .>1049
                     /product="neurotrophin-7"
     CDS             348. .1049
                     /note="neurotrophin family member; nerve growth factor
                     subfamily member; NT-7"
                     /codon_start=1
                     /product="neurotrophin-7"
```

```
                     /protein_id="AAC41272.1"
                     /db_xref="GI:3044091"
                     /translation="MRSLTLVLLILISIQAALIMGGHTQAQASANQHAATQNSPRLYS
                     QSKEDLHYDELIPTVDPKLFNKRRYRSPRVVFSDVITAEKEMGTPRRPRIRRKANDFL
                     HRGEYSVCDSEEHWVGNLTHATDLGGNEVMVLPHFRINNVVKKQLFYETTCRVKKPIG
                     APKPGQGASGVKAGTSSCRGIDSKHWNSYCTNTHTYVRALTSYKNQIAWRFIRINAAC
                     VCVLSRNSWRHGLKY"
BASE COUNT      356 a    301 c    259 g    302 t
ORIGIN


  Query Match           82.4%;  Score 328.6;  DB 4;  Length 1218;
  Best Local Similarity  89.0%;  Pred. No. 4.1e-75;
  Matches  355;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy       1 aaggccaacgacttcttgcatcgcggcgagtactctgtgtgtgacagcgaagagcactgg 60
             ||||| |||||||||| ||||||| || |||||||| |||||||||||||||||||||||
Db     636 AAGGCAAACGACTTCCTGCATCGTGGTGAGTACTCGGTGTGTGACAGCGAAGAGCACTGG 695

Qy      61 gttggcaacctgacccaagccacagacttacggggcaatgaagtcacggtgctgccacat 120
           |||||||||||||||| |||||||||||| |||||||||||||| |||||| ||||||
Db     696 GTTGGCAACCTGACCCATGCCACAGACTTAGGGGGCAATGAAGTCATGGTGCTACCACAT 755

Qy     121 gttcgcatcaacaacgtggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcg 180
           |||||||||||||||| || |||||||| | |||||||||||||| || ||||||  |
Db     756 TTTCGCATCAACAACGTTGTAAAGAAGCAGCTCTTCTACGAGACCACATGTCGTGTGAAG 815

Qy     181 aagcccatcggggcccccaagccgggtcaaggagtcagcggcgttaaagcaggaacctct 240
           || || || |||||||| ||||| |||||||||| ||| |||||||||| |||||||||
Db     816 AAACCTATAGGGGCCCCTAAGCCAGGTCAAGGAGCCAGTGGCGTTAAAGCGGGAACCTCT 875

Qy     241 agctgtcgtgggatcgacaacgagcactggaactcttattgcaccaacgtgcacacctttt 300
           |||||||||||  || |||| | ||||||||||||||||| |||||||||   |||||| |
Db     876 AGCTGTCGTGGCATTGACAGCAAGCACTGGAACTCTTACTGCACCAACACACACACCTAT 935

Qy     301 gtgcgggcgttaacgtcctacaaaaaccagattgcctggaggttcatccgaatcaacgcc 360
           ||||||||| |||||||||||||||||||| |||||||||||||||||||||||||||||
Db     936 GTGCGGGCGCTAACGTCCTACAAAAACCAGATCGCCTGGAGGTTCATCCGAATCAACGCC 995

Qy     361 gcttgcgtgtgcgtcctcagccgcaactcatggaggcat 399
           || || || || || |||||||| ||||| |||||||||
Db     996 GCATGTGTCTGTGTGCTCAGCCGTAACTCCTGGAGGCAT 1034


RESULT   3
XIPNE6G
LOCUS       XIPNE6G      1429 bp    DNA             VRT       02-FEB-1995
DEFINITION  Xiphophorus helleri neurotrophin-6 gene, complete cds.
ACCESSION   L36326
VERSION     L36326.1  GI:642669
KEYWORDS    neurotrophin-6.
SOURCE      Xiphophorus helleri (strain Rio Lancetilla Mexico) adult DNA.
  ORGANISM  Xiphophorus helleri
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Cyprinodontiformes; Poeciliidae; Xiphophorus.
REFERENCE   1  (bases 1 to 1429)
  AUTHORS   Gotz,R., Koster,R., Winkler,C., Raulf,F., Lottspeich,F., Schartl,M.
            and Thoenen,H.
  TITLE     Neurotrophin-6 is a new member of the nerve growth factor family
  JOURNAL   Nature 372 (6503), 266-269 (1994)
  MEDLINE   95059452
FEATURES             Location/Qualifiers
     source          1. .1429
                     /organism="Xiphophorus helleri"
                     /strain="Rio Lancetilla Mexico"
                     /db_xref="taxon:8084"
                     /dev_stage="adult"
     sig_peptide     143. .568
                     /note="putative"
     CDS             143. .1003
                     /codon_start=1
                     /product="neurotrophin-6"
                     /protein_id="AAA61921.1"
                     /db_xref="GI:642670"
                     /translation="MRSSLLVLLLLIGVQAVLNMGGGLARNPGAANHSAGQQETAAAR
                     GQLSQDQTSYQQHRTTHHRTKRTQSAASNMQNRTPVIGPSPAGSSPDPSSPVVDPKLF
                     SKRHYRPSPRVVFSEVIPSHDVLDGEGYDFERVRGLRVRRKAVSHTMHRGEYSVCDSI
                     NTWVNKTRATDMSGNEVTVLSHVTVNNKVKKQLFYETTCRSPTHRSSGIVIGGRSGGR
                     GGKQGSKTGNSGCRGIDSRYWNSHCTNTDIYVSALTVFKEQTAWRFIRINAACVCVLS
                     RNSWSRRPGH"
     mat_peptide     569. .1000
                     /evidence=experimental
                     /product="neurotrophin-6"
BASE COUNT      421 a    342 c    329 g    337 t
ORIGIN


  Query Match           32.4%;  Score 129.2;  DB 4;  Length 1429;
  Best Local Similarity  63.6%;  Pred. No. 2.2e-23;
  Matches  257;  Conservative    0;  Mismatches  123;  Indels   24;  Gaps    3;

Qy      11 acttcttgcatcgcggcgagtactctgtgtgtgacagcgaagagcactgggttggcaacc 70
           ||  | |||||||| || ||||||||||||||||||||||  | |  ||||||   |||
Db     582 ACACCATGCATCGAGGAGAGTACTCTGTGTGTGACAGTATAAATACCTGGGTG---AACA 638

Qy      71 tgacccaagccacagacttacggggcaatgaagtcacggtgctgccacatgttcgcatca 130
           ||| | |||||||||| |    || |||||||| || || ||  | || |||    |||
Db     639 AGACACGAGCCACAGACATGTCTGGAAATGAAGTGACAGTACTCTCCCACGTTACAGTCA 698

Qy     131 acaacgtggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcgaagccc---- 186
           ||||| ||| ||||| ||| | || || |||||||| ||  |     ||| || |
Db     699 ACAACAAGGTAAAGAAACAGCTTTTTTATGAGACCACCTGTAGATCCCCGACGCACAGGA 758

Qy     187 --------------atcggggcccccaagccgggtcaaggagtca---gcggcgttaaag 229
                         |||||||  |        || | ||| |  |     |||   ||
Db     759 GTTCTGGAATCGTAATCGGGGGACGATCTGGAGGACGAGGTGGAAAGCAAGGCTCCAAGA 818

Qy     230 caggaacctctagctgtcgtgggatcgacaacgagcactggaactcttattgcaccaacg 289
           |||| | |||  | ||||| || || |||| |    ||||||||||  | |||||||||
Db     819 CAGGCAACTCGGGTTGTCGAGGCATTGACAGCCGCTACTGGAACTCCCACTGCACCAACA 878

Qy     290 tgcacacctttgtgcgggcgttaacgtcctacaaaaaccagattgcctggaggttcatcc 349
           |||  | |||  | ||  | ||   || |||  | ||||  ||||||  | |||||||
Db     879 CAGACATATATGTAAGCGCCCTGACCGTCTTCAAGGAACAGACAGCCTGGCGTTTCATCC 938

Qy     350 gaatcaacgccgcttgcgtgtgcgtcctcagccgcaactcatgg 393
           | |||||||| || || ||||| || |||||||| || || |||
Db     939 GCATCAACGCTGCATGTGTGTGTTCTCAGCCGGAATTCTTGG 982


RESULT   4
XIPNE6R
LOCUS       XIPNE6R      1429 bp    mRNA            VRT       02-FEB-1995
DEFINITION  Xiphophorus helleri neurotrophin-6 mRNA, complete cds.
ACCESSION   L36325
VERSION     L36325.1  GI:642671
KEYWORDS    neurotrophin-6.
SOURCE      Xiphophorus helleri (strain Rio Lancetilla Mexico) adult cDNA to
            mRNA.
  ORGANISM  Xiphophorus helleri
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Cyprinodontiformes; Poeciliidae; Xiphophorus.
REFERENCE   1  (bases 1 to 1429)
  AUTHORS   Gotz,R., Koster,R., Winkler,C., Raulf,F., Lottspeich,F., Schartl,M.
            and Thoenen,H.
  TITLE     Neurotrophin-6 is a new member of the nerve growth factor family
  JOURNAL   Nature 372 (6503), 266-269 (1994)
  MEDLINE   95059452
FEATURES             Location/Qualifiers
     source          1. .1429
                     /organism="Xiphophorus helleri"
                     /strain="Rio Lancetilla Mexico"
```

```
                     /db_xref="taxon:8084"
                     /dev_stage="adult"
     sig_peptide     143. .568
                     /note="putative"
     CDS             143. .1003
                     /codon_start=1
                     /product="neurotrophin-6"
                     /protein_id="AAA61922.1"
                     /db_xref="GI:642672"
                     /translation="MRSSLLVLLLLIGVQAVLNMGGGLARNPGAANHSAGQQETAAAR
                     GQLSQDQTSYQQHRTTHHRTKRTQSAASNMQNRTPVIGPSPAGSSPDPSSPVVDPKLF
                     SKRHYRPSPRVVFSEVIPSHDVLDGEGYDFERVRGLRVRRKAVSHTMHRGEYSVCDSI
                     NTWVNKTRATDMSGNEVTVLSHVTVNNKVKKQLFYETTCRSPTHRSSGIVIGGRSGGR
                     GGKQGSKTGNSGCRGIDSRYWNSHCTNTDIYVSALTVFKEQTAWRFIRINAACVCVLS
                     RNSWSRRPGH"
     mat_peptide     569. .1000
                     /evidence=experimental
                     /product="neurotrophin-6"
BASE COUNT      421 a    342 c    329 g    337 t
ORIGIN
```

Query Match 32.4%; Score 129.2; DB 4; Length 1429;
Best Local Similarity 63.6%; Pred. No. 2.2e-23;
Matches 257; Conservative 0; Mismatches 123; Indels 24; Gaps 3;

```
Qy      11 acttcttgcatcgcggcgagtactctgtgtgtgacagcgaagagcactgggttggcaacc 70
           ||  | |||||||  || ||||||||||||||||||||||  | |   ||||||    |||
Db     582 ACACCATGCATCGAGGAGAGTACTCTGTGTGTGACAGTATAAATACCTGGGTG---AACA 638

Qy      71 tgacccaagccacagacttacggggcaatgaagtcacggtgctgccacatgttcgcatca 130
           ||| | ||||||||||| |    || ||||||||| || || ||  | || |||    |||
Db     639 AGACACGAGCCACAGACATGTCTGGAAATGAAGTGACAGTACTCTCCCACGTTACAGTCA 698

Qy     131 acaacgtggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcgaagccc---- 186
           |||||  ||| ||||| ||| | || || |||||||| ||  |     ||| || |
Db     699 ACAACAAGGTAAAGAAACAGCTTTTTTATGAGACCACCTGTAGATCCCCGACGCACAGGA 758

Qy     187 --------------atcggggccccccaagccgggtcaaggagtca---gcggcgttaaag 229
                         |||||||  |        || | ||| |  |     |||   ||
Db     759 GTTCTGGAATCGTAATCGGGGGACGATCTGGAGGACGAGGTGGAAAGCAAGGCTCCAAGA 818

Qy     230 caggaacctctagctgtcgtgggatcgacaacgagcactggaactcttattgcaccaacg 289
           |||| | |||  | ||||| || || |||| |    ||||||||||  | |||||||||
Db     819 CAGGCAACTCGGGTTGTCGAGGCATTGACAGCCGCTACTGGAACTCCCACTGCACCAACA 878

Qy     290 tgcacacctttgtgcgggcgttaacgtcctacaaaaaccagattgcctggaggttcatcc 349
           |||  | |||  | ||  | ||   || |||  | ||||  ||||||  | |||||||
Db     879 CAGACATATATGTAAGCGCCCTGACCGTCTTCAAGGAACAGACAGCCTGGCGTTTCATCC 938

Qy     350 gaatcaacgccgcttgcgtgtgcgtcctcagccgcaactcatgg 393
           | ||||||||  || ||  ||||| ||  |||||||| || || |||
Db     939 GCATCAACGCTGCATGTGTGTGTGTTCTCAGCCGGAATTCTTGG 982
```

```
RESULT   5
A46744
LOCUS       A46744       1429 bp    DNA             PAT       07-MAR-1997
DEFINITION  Sequence 1 from Patent WO9526363.
ACCESSION   A46744
VERSION     A46744.1  GI:2300839
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1429)
  AUTHORS   Goetz,R.G., Thoenen,H., Lottspeich,F. and Schartl,M.
  TITLE     NEUROTROPHIN-6: A NEW MEMBER OF THE NEUROTROPHIN FAMILY
  JOURNAL   Patent: WO 9526363-A 1 05-OCT-1995;
            MAX PLANCK GESELLSCHAFT (DE)
FEATURES             Location/Qualifiers
     source          1. .1429
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     CDS             143. .1003
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAA02942.1"
                     /db_xref="GI:2300840"
                     /translation="MRSSLLVLLLLIGVQAVLNMGGGLARNPGAANHSAGQQETAAAR
                     GQLSQDQTSYQQHRTTHHRTKRTQSAASNMQNRTPVIGPSPAGSSPDPSSPVVDPKLF
                     SKRHYRPSPRVVFSEVIPSHDVLDGEGYDFERVRGLRVRRKAVSHTMHRGEYSVCDSI
                     NTWVNKTRATDMSGNEVTVLSHVTVNNKVKKQLFYETTCRSPTHRSSGIVIGGRSGGR
                     GGKQGSKTGNSGCRGIDSRYWNSHCTNTDIYVSALTVFKEQTAWRFIRINAACVCVLS
                     RNSWSRRPGH"
BASE COUNT      421 a    342 c    329 g    337 t
ORIGIN
```

Query Match 32.4%; Score 129.2; DB 5; Length 1429;
Best Local Similarity 63.6%; Pred. No. 2.2e-23;
Matches 257; Conservative 0; Mismatches 123; Indels 24; Gaps 3;

```
Qy      11 acttcttgcatcgcggcgagtactctgtgtgtgacagcgaagagcactgggttggcaacc 70
           ||  | |||||||  || ||||||||||||||||||||||  | |   ||||||    |||
Db     582 ACACCATGCATCGAGGAGAGTACTCTGTGTGTGACAGTATAAATACCTGGGTG---AACA 638

Qy      71 tgacccaagccacagacttacggggcaatgaagtcacggtgctgccacatgttcgcatca 130
           ||| | ||||||||||| |    || ||||||||| || || ||  | || |||    |||
Db     639 AGACACGAGCCACAGACATGTCTGGAAATGAAGTGACAGTACTCTCCCACGTTACAGTCA 698

Qy     131 acaacgtggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcgaagccc---- 186
           |||||  ||| ||||| ||| | || || |||||||| ||  |     ||| || |
Db     699 ACAACAAGGTAAAGAAACAGCTTTTTTATGAGACCACCTGTAGATCCCCGACGCACAGGA 758

Qy     187 --------------atcggggccccccaagccgggtcaaggagtca---gcggcgttaaag 229
                         |||||||  |        || | ||| |  |     |||   ||
Db     759 GTTCTGGAATCGTAATCGGGGGACGATCTGGAGGACGAGGTGGAAAGCAAGGCTCCAAGA 818

Qy     230 caggaacctctagctgtcgtgggatcgacaacgagcactggaactcttattgcaccaacg 289
           |||| | |||  | ||||| || || |||| |    ||||||||||  | |||||||||
Db     819 CAGGCAACTCGGGTTGTCGAGGCATTGACAGCCGCTACTGGAACTCCCACTGCACCAACA 878

Qy     290 tgcacacctttgtgcgggcgttaacgtcctacaaaaaccagattgcctggaggttcatcc 349
           |||  | |||  | ||  | ||   || |||  | ||||  ||||||  | |||||||
Db     879 CAGACATATATGTAAGCGCCCTGACCGTCTTCAAGGAACAGACAGCCTGGCGTTTCATCC 938

Qy     350 gaatcaacgccgcttgcgtgtgcgtcctcagccgcaactcatgg 393
           | ||||||||  || ||  ||||| ||  |||||||| || || |||
Db     939 GCATCAACGCTGCATGTGTGTGTGTTCTCAGCCGGAATTCTTGG 982
```

```
RESULT   6
XIPNRTN6A
LOCUS       XIPNRTN6A    1700 bp    DNA             VRT       02-FEB-1995
DEFINITION  Xiphpophorus maculatus neurotrophin-6 gene, complete cds.
ACCESSION   L36942
VERSION     L36942.1  GI:642673
KEYWORDS    heparin binding protein; nerve growth factor; neurotrophin-6.
SOURCE      Xiphophorus maculatus DNA.
  ORGANISM  Xiphophorus maculatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Cyprinodontiformes; Poeciliidae; Xiphophorus.
REFERENCE   1  (bases 1 to 1700)
  AUTHORS   Gotz,R., Koster,R., Winkler,C., Raulf,F., Lottspeich,F., Schartl,M.
            and Thoenen,H.
  TITLE     Neurotrophin-6 is a new member of the nerve growth factor family
  JOURNAL   Nature 372 (6503), 266-269 (1994)
  MEDLINE   95059452
FEATURES             Location/Qualifiers
     source          1. .1700
                     /organism="Xiphophorus maculatus"
                     /db_xref="taxon:8083"
     sig_peptide     326. .751
```

```
                /evidence=experimental
     CDS        326. .1186
                /standard_name="nerve growth factor"
                /note="putative"
                /codon_start=1
                /product="neurotrophin-6"
                /protein_id="AAA61923.1"
                /db_xref="GI:642674"
                /translation="MRSSLLVLLLLIGVQAVLNMGGGLARNPGAANHSAGQQETAAAR
                GQLSQDQTSYQQHRTTHHRTKRTQSAASNMQNRTPVIGPSPAGSSPDPSSPVVDPKLF
                SKRHYRPSPRVVFSEVIPSHDVLDGEGYDFERVRGLRVRRKAVSHTMHRGEYSVCDSI
                NTWVNKTRATDMSGNEVTVLSHVTVNNKVKKQLFYETTCRSPTHRSSGIVIGGRSGGR
                GGKQGSKTGNSGCRGIDSRYWNSHCTNTDIYVSALTVFKEQTAWRFIRINAACVCVLS
                RNSWSRRPGH"
     mat_peptide 752. .1183
                /standard_name="nerve growth factor"
                /evidence=experimental
                /product="neurotrophin-6"
BASE COUNT      501 a    400 c    356 g    443 t
ORIGIN
```

```
  Query Match           32.0%;  Score 127.6;  DB 4;  Length 1700;
  Best Local Similarity  63.4%;  Pred. No. 5.7e-23;
  Matches  256;  Conservative    0;  Mismatches  124;  Indels   24;  Gaps    3;

Qy      11 acttcttgcatcgcggcgagtactctgtgtgtgacagcgaagagcactgggttggcaacc 70
           ||  | ||||||| || ||||||||||||||||||||   | |   ||||||    |||
Db     765 ACACCATGCATCGAGGAGAGTACTCTGTGTGTGACAGTATAAATACCTGGGTG---AACA 821

Qy      71 tgacccaagccacagacttacggggcaatgaagtcacggtgctgccacatgttcgcatca 130
           ||| | ||||||||||| |    || |||||||| || || ||  | || |||    |||
Db     822 AGACACGAGCCACAGACATGTCTGGAAATGAAGTGACAGTACTCTCCCACGTTACAGTCA 881

Qy     131 acaacgtggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcgaagccc---- 186
           |||||  ||| ||||| ||| | || || |||||||| ||  |     |||  | |
Db     882 ACAACAAGGTAAAGAAACAGCTTTTTTATGAGACCACCTGTAGATCCCCGACACACAGGA 941

Qy     187 --------------atcggggccccccaagccgggtcaaggagtca---gcggcgttaaag 229
                         |||||||  |        || | ||| |  |    |||   ||
Db     942 GTTCTGGAATCGTAATCGGGGGACGATCTGGAGGACGAGGTGGAAAGCAAGGCTCCAAGA 1001

Qy     230 caggaacctctagctgtcgtgggatcgacaacgagcactggaactcttattgcaccaacg 289
           |||| | |||  | ||||| || || |||| |    ||||||||||  | |||||||||
Db    1002 CAGGCAACTCAGGTTGTCGAGGCATTGACAGCCGCTACTGGAACTCCCACTGCACCAACA 1061

Qy     290 tgcacacctttgtgcgggcgttaacgtcctacaaaaaccagattgcctggaggttcatcc 349
           |||  | |||  | ||  | ||   || |||  | ||||  ||||||  | |||||||
Db    1062 CAGACATATATGTAAGCGCTCTGACCGTCTTCAAGGAACAGACAGCCTGGCGTTTCATCC 1121

Qy     350 gaatcaacgccgcttgcgtgtgcgtcctcagccgcaactcatgg 393
           | |||||||| || || ||||| || |||||||| || || |||
Db    1122 GCATCAACGCTGCATGTGTGTGTGTTCTCAGCCGGAATTCTTGG 1165
```

```
RESULT   7
A46746
LOCUS       A46746       2273 bp    DNA             PAT       07-MAR-1997
DEFINITION  Sequence 3 from Patent WO9526363.
ACCESSION   A46746
VERSION     A46746.1  GI:2300841
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2273)
  AUTHORS   Goetz,R.G., Thoenen,H., Lottspeich,F. and Schartl,M.
  TITLE     NEUROTROPHIN-6: A NEW MEMBER OF THE NEUROTROPHIN FAMILY
  JOURNAL   Patent: WO 9526363-A 3 05-OCT-1995;
            MAX PLANCK GESELLSCHAFT (DE)
FEATURES             Location/Qualifiers
     source          1. .2273
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      630 a    531 c    446 g    666 t
ORIGIN
```

```
  Query Match           32.0%;  Score 127.6;  DB 5;  Length 2273;
  Best Local Similarity  63.4%;  Pred. No. 5.5e-23;
  Matches  256;  Conservative    0;  Mismatches  124;  Indels   24;  Gaps    3;

Qy      11 acttcttgcatcgcggcgagtactctgtgtgtgacagcgaagagcactgggttggcaacc 70
           ||  | ||||||| || ||||||||||||||||||||   | |   ||||||    |||
Db    1304 ACACCATGCATCGAGGAGAGTACTCTGTGTGTGACAGTATAAATACCTGGGTG---AACA 1360

Qy      71 tgacccaagccacagacttacggggcaatgaagtcacggtgctgccacatgttcgcatca 130
           ||| | ||||||||||| |    || |||||||| || || ||  | || |||    |||
Db    1361 AGACACGAGCCACAGACATGTCTGGAAATGAAGTGACAGTACTCTCCCACGTTACAGTCA 1420

Qy     131 acaacgtggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcgaagccc---- 186
           |||||  ||| ||||| ||| | || || |||||||| ||  |     |||  | |
Db    1421 ACAACAAGGTAAAGAAACAGCTTTTTTATGAGACCACCTGTAGATCCCCGACACACAGGA 1480

Qy     187 --------------atcggggccccccaagccgggtcaaggagtca---gcggcgttaaag 229
                         |||||||  |        || | ||| |  |    |||   ||
Db    1481 GTTCTGGAATCGTAATCGGGGGACGATCTGGAGGACGAGGTGGAAAGCAAGGCTCCAAGA 1540

Qy     230 caggaacctctagctgtcgtgggatcgacaacgagcactggaactcttattgcaccaacg 289
           |||| | |||  | ||||| || || |||| |    ||||||||||  | |||||||||
Db    1541 CAGGCAACTCAGGTTGTCGAGGCATTGACAGCCGCTACTGGAACTCCCACTGCACCAACA 1600

Qy     290 tgcacacctttgtgcgggcgttaacgtcctacaaaaaccagattgcctggaggttcatcc 349
           |||  | |||  | ||  | ||   || |||  | ||||  ||||||  | |||||||
Db    1601 CAGACATATATGTAAGCGCTCTGACCGTCTTCAAGGAACAGACAGCCTGGCGTTTCATCC 1660

Qy     350 gaatcaacgccgcttgcgtgtgcgtcctcagccgcaactcatgg 393
           | |||||||| || || ||||| || |||||||| || || |||
Db    1661 GCATCAACGCTGCATGTGTGTGTGTTCTCAGCCGGAATTCTTGG 1704
```

```
RESULT   8
XMNGFAA
LOCUS       XMNGFAA      720 bp    DNA             VRT       20-JUL-1993
DEFINITION  X.maculatus NGF gene for nerve growth factor.
ACCESSION   X59941 S40498
VERSION     X59941.1  GI:65277
KEYWORDS    nerve growth factor.
SOURCE      southern platyfish.
  ORGANISM  Xiphophorus maculatus
            Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
            Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
            Atherinomorpha; Cyprinodontiformes; Cyprinodontoidei; Poeciliidae;
            Xiphophorus.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   Goetz,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUN-1991) R. Goetz, Max Planck Inst for Psychiatry,
            Dept of Neurochemistry, Am Klopferspitz 18A, D-8033 Martinsried,
            FRG
REFERENCE   2  (bases 1 to 720)
  AUTHORS   Gotz,R., Raulf,F. and Schartl,M.
  TITLE     Brain-derived neurotrophic factor is more highly conserved in
            structure and function than nerve growth factor during vertebrate
            evolution
  JOURNAL   J. Neurochem. 59 (2), 432-442 (1992)
  MEDLINE   92333301
FEATURES             Location/Qualifiers
     source          1. .720
                     /organism="Xiphophorus maculatus"
                     /isolate="origin Rio Usumacinta"
                     /db_xref="taxon:8083"
                     /clone="A5.2"
     gene            121. .705
                     /gene="NGF"
     CDS             121. .705
```

```
                     /gene="NGF"
                     /codon_start=1
                     /product="nerve growth factor"
                     /protein_id="CAA42566.1"
                     /db_xref="GI:65278"
                     /db_xref="SWISS-PROT:P34129"
                     /translation="MRSSMLVLFLIFSAQAVAPIIGVLCSVTTAQQDHPTSIPTVDPK
                     LFNKRRHLSPRVLFSSQPPDAEPAGGQGVSRRTRRQPQHRGVYSVCESVSVWVGNKTK
                     ATDISGKEVTVLPYVNINNVKKKQYFFETTCHSPPSGGSRCLGIDARHWNSHCTNSHT
                     FVRALTSSENQVAWRLIRINVACVCVLSRKSWQH"
     mat_peptide     358. .702
                     /gene="NGF"
                     /product="nerve growth factor"
BASE COUNT      169 a    196 c    181 g    174 t
ORIGIN

  Query Match             31.0%;  Score 123.6;  DB 4;  Length 720;
  Best Local Similarity   62.3%;  Pred. No. 7e-22;
  Matches  238;  Conservative    0;  Mismatches   99;  Indels   45;  Gaps    1;

Qy      18 gcatcgcggcgagtactctgtgtgtgacagcgaagagcactgggttggcaacctgaccca 77
           ||| || || | |||||| |||||||| || |       |||||| ||||||   ||| |
Db     366 GCACCGGGGGGTGTACTCGGTGTGTGAGAGTGTTAGTGTCTGGGTGGGCAACAAAACCAA 425

Qy      78 agccacagacttacggggcaatgaagtcacggtgctgccacatgttcgcatcaacaacgt 137
           |||||||||| |    ||||| || || || ||||| ||| ||||   ||| ||||| ||
Db     426 AGCCACAGACATCTCAGGCAAAGAGGTGACAGTGCTCCCATATGTGAACATAAACAATGT 485

Qy     138 ggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcgaagcccatcggggcccc 197
           ||||||| |||   ||||  ||||| ||||| |
Db     486 TAAGAAGAAACAGTATTTCTTTGAGACGACGTGTCA---------------------- 521

Qy     198 caagccgggtcaaggagtcagcggcgttaaagcaggaacctctagctgtcgtgggatcga 257
                           | ||  |  | | |||  ||| || |||   || || ||
Db     522 --------------------CAGCCCTCCATCTGGAGGCTCAAGATGTTTAGGAATTGA 560

Qy     258 caacgagcactggaactcttattgcaccaacgtgcacacctttgtgcgggcgttaacgtc 317
           |     ||||||||||||  | |||||||||  |||||| || || || ||| | || ||
Db     561 CGCAAGGCACTGGAACTCCCACTGCACCAACTCGCACACTTTCGTCCGAGCGCTCACTTC 620

Qy     318 ctacaaaaaccagattgcctggaggttcatccgaatcaacgccgcttgcgtgtgcgtcct 377
           | | | |||||+ | || |||||| |||| || ||||||| || || |||||||| ||
Db     621 ATCCGAGAACCAGGTGGCTTGGAGGCTCATTCGGATCAACGTGGCGTGTGTGTGCGTGCT 680

Qy     378 cagccgcaactcatggaggcat 399
           ||||||||| || |||  ||||
Db     681 CAGCCGCAAATCGTGGCAGCAT 702


RESULT   9
PIGNGFB
LOCUS       PIGNGFB       763 bp    DNA             MAM       02-SEP-1994
DEFINITION  Pig nerve growth factor B (NGFB) gene, partial cds.
ACCESSION   L31898
VERSION     L31898.1  GI:476732
KEYWORDS    nerve growth factor B.
SOURCE      Sus scrofa (strain Large White) DNA.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 763)
  AUTHORS   Lahbib-Mansais,Y., Mellink,C., Yerle,M. and Gellin,J.
  TITLE     A new marker (NGFB) on pig chromosome 4, isolated by using
            consensus sequence conserved among species
  JOURNAL   Cytogenet. Cell Genet. 67, 120-125 (1994)
  MEDLINE   94313891
FEATURES             Location/Qualifiers
     source          1. .763
                     /organism="Sus scrofa"
                     /strain="Large White"
                     /db_xref="taxon:9823"
                     /cell_type="lymphocyte"
                     /tissue_type="blood"
                     /map="4q1.6-q2.3"
     gene            1. .692
                     /gene="NGFB"
     CDS             <1. .692
                     /gene="NGFB"
                     /codon_start=3
                     /product="nerve growth factor B"
                     /protein_id="AAA21301.1"
                     /db_xref="GI:533771"
                     /translation="LIGIQAEPHTESNVPAGHAIPQAHWTKLQHSLDTALRRAHSAPA
                     GANSARVAGQTRNITVDPKLFKKRRLRSPRVLFSTQPPPVAADTQDPDLEASGAASFN
                     RTHRSKRSSSHPVFHRGEFSVCDSVSVWVGDKTTATDIKGKEVMVLGEVNINNSVFKQ
                     YFFETKCRDPNPVDSGCRGIDSKHWNSYCTTTHTFVKALTMDGKQAAWRFIRIDTACV
                     CVLSRKAGRRA"
BASE COUNT      170 a    256 c    212 g    125 t
ORIGIN

  Query Match             26.0%;  Score 103.8;  DB 3;  Length 763;
  Best Local Similarity   58.6%;  Pred. No. 9.6e-17;
  Matches  229;  Conservative    0;  Mismatches  117;  Indels   45;  Gaps    1;

Qy       5 ccaacgacttcttgcatcgcggcgagtactctgtgtgtgacagcgaagagcactgggttg 64
           || ||  | | || || || || |||| ||| ||||| |||||||        ||||| |
Db     337 CCCACCCCGTTTTCCACCGGGGGGAGTTCTCGGTGTGCGACAGCGTCAGCGTGTGGGTGG 396

Qy      65 gcaacctgacccaagccacagacttacggggcaatgaagtcacggtgctgccacatgttc 124
           |  ||  ||||   ||||| ||| |   |||||| || || | |||| ||  | | ||
Db     397 GGGACAAGACCACTGCCACGGACATCAAGGGCAAGGAGGTGATGGTGTTGGGAGAGGTGA 456

Qy     125 gcatcaacaacgtggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcgaagc 184
           |||||||||  |||   || |||   || |  ||||||| |||||| |   | || |
Db     457 ATATCAACAACAGCGTGTTTAAACAGTACTTTTTTGAGACCAAGTGCCGGGACCCCAATC 516

Qy     185 ccatcggggccccaagccgggtcaaggagtcagcggcgttaaagcaggaacctctagct 244
           || | |   |                                              | |
Db     517 CCGTGGACAGCG----------------------------------------------GGT 531

Qy     245 gtcgtgggatcgacaacgagcactggaactcttattgcaccaacgtgcacacctttgtgc 304
           | || || ||||||    |||||||||||||| ||||| ||||     ||||||||||
Db     532 GCCGGGGCATCGACTCAAAGCACTGGAACTCGTATTGTACCACAACCCACACCTTTGTCA 591

Qy     305 gggcgttaacgtcctacaaaaaccagattgcctggaggttcatccgaatcaacgccgctt 364
           |||| | ||     ||   || ||| ||||||| |||| ||||||||| || | || |
Db     592 AGGCGCTGACCATGGACGGCAAGCAGGCTGCCTGGCGGTTTATCCGAATCGACACGGCCT 651

Qy     365 gcgtgtgcgtcctcagccgcaactcatggag 395
           |||||||||| |||||| | ||  |  ||||
Db     652 GCGTGTGCGTGCTCAGCAGGAAGGCGGGGAG 682


RESULT  10
MUSGFN4
LOCUS       MUSGFN4       1123 bp    DNA             ROD       30-MAR-1994
DEFINITION  Mouse nerve growth factor gene, exon 4.
ACCESSION   M17298
VERSION     M17298.1  GI:193493
KEYWORDS    alternative splicing; nerve growth factor.
SEGMENT     4 of 4
SOURCE      Mus musculus (strain C57/BL6) submaxillary gland DNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1123)
  AUTHORS   Selby,M.J.
  JOURNAL   Unpublished (1987)
REFERENCE   2  (bases 814 to 1097)
  AUTHORS   Selby,M.J., Edwards,R., Sharp,F. and Rutter,W.J.
  TITLE     Mouse nerve growth factor gene: Structure and expression
  JOURNAL   Mol. Cell. Biol. 7, 3057-3064 (1987)
  MEDLINE   88038855
COMMENT     Draft entry and computer-readable sequence for [2] kindly provided
```

```
          by M.J.Selby, 13-OCT-1987.
FEATURES             Location/Qualifiers
     source          1. .1123
                     /organism="Mus musculus"
                     /strain="C57/BL6"
                     /db_xref="taxon:10090"
                     /tissue_type="submaxillary gland"
     mRNA            join(M17295.1:481. .646,M17297.1:974. .1097,34. .928)
                     /gene="NGF"
                     /note="type C"
     gene            join(M17295.1:481. .927,M17296.1:1. .2185,M17297.1:1. .1208,
                     1. .928)
                     /gene="NGF"
     mRNA            join(M17295.1:789. .821,M17297.1:974. .1097,34. .928)
                     /gene="NGF"
                     /note="type B"
     mRNA            join(M17295.1:789. .821,M17296.1:1379. .1507,
                     M17297.1:974. .1097,34. .928)
                     /gene="NGF"
                     /note="type A"
     CDS             join(M17296.1:1446. .1507,M17297.1:974. .1097,34. .771)
                     /gene="NGF"
                     /note="alternative precursor"
                     /codon_start=1
                     /product="nerve growth factor"
                     /protein_id="AAA37687.1"
                     /db_xref="GI:467311"
                     /translation="MLCLKPVKLGSLEVGHGQHGGVLACGRAVQGAGWHAGPKLTSVS
                     GPNKGFAKDAAFYTGRSEVHSVMSMLFYTLITAFLIGVQAEPYTDSNVPEGDSVPEAH
                     WTKLQHSLDTALRRARSAPTAPIAARVTGQTRNITVDPRLFKKRRLHSPRVLFSTQPP
                     PTSSDTLDLDFQAHGTIPFNRTHRSKRSSTHPVFHMGEFSVCDSVSVWVGDKTTATDI
                     KGKEVTVLAEVNINNSVFRQYFFETKCRASNPVESGCRGIDSKHWNSYCTTTHTFVKA
                     LTTDEKQAAWRFIRIDTACVCVLSRKATRRG"
     CDS             join(M17296.1:1446. .1507,M17297.1:974. .1097,34. .771)
                     /gene="NGF"
                     /note="alternative precursor A"
                     /codon_start=1
                     /product="nerve growth factor"
                     /protein_id="AAA37686.1"
                     /db_xref="GI:387171"
                     /translation="MLCLKPVKLGSLEVGHGQHGGVLACGRAVQGAGWHAGPKLTSVS
                     GPNKGFAKDAAFYTGRSEVHSVMSMLFYTLITAFLIGVQAEPYTDSNVPEGDSVPEAH
                     WTKLQHSLDTALRRARSAPTAPIAARVTGQTRNITVDPRLFKKRRLHSPRVLFSTQPP
                     PTSSDTLDLDFQAHGTIPFNRTHRSKRSSTHPVFHMGEFSVCDSVSVWVGDKTTATDI
                     KGKEVTVLAEVNINNSVFRQYFFETKCRASNPVESGCRGIDSKHWNSYCTTTHTFVKA
                     LTTDEKQAAWRFIRIDTACVCVLSRKATRRG"
     mRNA            join(M17297.1:813. .1097,34. .928)
                     /gene="NGF"
                     /note="type D"
     intron          <1. .33
                     /gene="NGF"
     exon            34. .928
                     /gene="NGF"
                     /note="alternative"
                     /number=5
     mat_peptide     409. .762
                     /gene="NGF"
                     /product="nerve growth factor"
BASE COUNT      291 a    332 c    240 g    260 t
ORIGIN      About 6 kb after segment 3.

  Query Match           25.0%;  Score 99.6;  DB 12;  Length 1123;
  Best Local Similarity   58.4%;  Pred. No. 1.1e-15;
  Matches  223;  Conservative    0;  Mismatches  114;  Indels   45;  Gaps    1;

Qy       5 ccaacgacttcttgcatcgcggcgagtactctgtgtgtgacagcgaagagcactgggttg 64
           || ||    |||| ||    || |||| ||| |||||||||||| |       |||||||
Db     416 CCCACCCAGTCTTCCACATGGGGGAGTTCTCAGTGTGTGACAGTGTCAGTGTGTGGGTTG 475

Qy      65 gcaacctgacccaagccacagacttacggggcaatgaagtcacggtgctgccacatgttc 124
           |  |   ||||  |||||||||| |   |||||| || || || |||||| |  | ||
Db     476 GAGATAAGACCACAGCCACAGACATCAAGGGCAAGGAGGTGACAGTGCTGGCCGAGGTGA 535

Qy     125 gcatcaacaacgtggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcgaagc 184
           ||| ||||||   ||    |  |||   || |  ||||||| |||||| |  || || |
Db     536 ACATTAACAACAGTGTATTCAGACAGTACTTTTTTGAGACCAAGTGCCGAGCCTCCAATC 595

Qy     185 ccatcggggcccccaagccgggtcaaggagtcagcggcgttaaagcaggaacctctagct 244
           |  | | |                                                | | |
Db     596 CTGTTGAGAC----------------------------------------------TGGGT 610

Qy     245 gtcgtgggatcgacaacgagcactggaactcttattgcaccaacgtgcacacctttgtgc 304
           | || || ||||||  | | ||||||||||| || |||||||     ||||||||  ||
Db     611 GCCGGGGCATCGACTCCAAACACTGGAACTCATACTGCACCACGACTCACACCTTCGTCA 670

Qy     305 gggcgttaacgtcctacaaaaaccagattgcctggaggttcatccgaatcaacgccgctt 364
           |||||| ||  |  |  | || |||  ||||||||||||||||||  ||  || | || |
Db     671 AGGCGTTGACAACAGATGAGAAGCAGGCTGCCTGGAGGTTCATCCGGATAGACACAGCCT 730

Qy     365 gcgtgtgcgtcctcagccgcaa 386
           | ||||| || |||||| | ||
Db     731 GTGTGTGTGTGCTCAGCAGGAA 752


RESULT  11
MMNGF1
LOCUS       MMNGF1       1176 bp    mRNA            ROD       27-MAR-1995
DEFINITION  Mouse mRNA encoding nerve growth factor (NGF).
ACCESSION   V00836
VERSION     V00836.1  GI:53364
KEYWORDS    complementary DNA; nerve growth factor.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1176)
  AUTHORS   Scott,J., Selby,M., Urdea,M., Quiroga,M., Bell,G.I. and Rutter,W.J.
  TITLE     Isolation and nucleotide sequence of a cDNA encoding the precursor
            of mouse nerve growth factor
  JOURNAL   Nature 302 (5908), 538-540 (1983)
  MEDLINE   83167518
COMMENT     Data kindly reviewed (04-JUL-1983) by J. Scott.
FEATURES             Location/Qualifiers
     source          1. .1176
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
     mRNA            1. .1176
                     /note="messenger RNA"
     CDS             96. .1019
                     /note="precursor of NGF"
                     /codon_start=1
                     /protein_id="CAA24221.1"
                     /db_xref="GI:53365"
                     /db_xref="MGD:MGI:97321"
                     /db_xref="SWISS-PROT:P01139"
                     /translation="MLCLKPVKLGSLEVGHGQHGGVLACGRAVQGAGWHAGPKLTSVS
                     GPNKGFAKDAAFYTGRSEVHSVMSMLFYTLITAFLIGVQAEPYTDSNVPEGDSVPEAH
                     WTKLQHSLDTALRRARSAPTAPIAARVTGQTRNITVDPRLFKKRRLHSPRVLFSTQPP
                     PTSSDTLDLDFQAHGTIPFNRTHRSKRSSTHPVFHMGEFSVCDSVSVWVGDKTTATDI
                     KGKEVTVLAEVNINNSVFRQYFFETKCRASNPVESGCRGIDSKHWNSYCTTTHTFVKA
                     LTTDEKQAAWRFIRIDTACVCVLSRKATRRG"
     mat_peptide     657. .1010
                     /product="mature NGF"
     polyA_site      1176
                     /note="polyA addition site"
BASE COUNT      283 a    330 c    295 g    268 t
ORIGIN

  Query Match           25.0%;  Score 99.6;  DB 12;  Length 1176;
  Best Local Similarity   58.4%;  Pred. No. 1.1e-15;
  Matches  223;  Conservative    0;  Mismatches  114;  Indels   45;  Gaps    1;

Qy       5 ccaacgacttcttgcatcgcggcgagtactctgtgtgtgacagcgaagagcactgggttg 64
           || ||    |||| ||    || |||| ||| |||||||||||| |       |||||||
```

```
Db    664 CCCACCCAGTCTTCCACATGGGGGAGTTCTCAGTGTGTGACAGTGTCAGTGTGTGGGTTG 723

Qy     65 gcaacctgacccaagccacagacttacggggcaatgaagtcacggtgctgccacatgttc 124

Db    724 GAGATAAGACCACAGCCACAGACATCAAGGGCAAGGAGGTGACAGTGCTGGCCGAGGTGA 783

Qy    125 gcatcaacaacgtggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcgaagc 184

Db    784 ACATTAACAACAGTGTATTCAGACAGTACTTTTTTGAGACCAAGTGCCGAGCCTCCAATC 843

Qy    185 ccatcggggcccccaagccgggtcaaggagtcagcggcgttaaagcaggaacctctagct 244

Db    844 CTGTTGAGAG----------------------------------------------TGGGT 858

Qy    245 gtcgtgggatcgacaacgagcactggaactcttattgcaccaacgtgcacacctttgtgc 304

Db    859 GCCGGGGCATCGACTCCAAACACTGGAACTCATACTGCACCACGACTCACACCTTCGTCA 918

Qy    305 gggcgttaacgtcctacaaaaaccagattgcctggaggttcatccgaatcaacgccgctt 364

Db    919 AGGCGTTGACAACAGATGAGAAGCAGGCTGCCTGGAGGTTCATCCGGATAGACACAGCCT 978

Qy    365 gcgtgtgcgtcctcagccgcaa 386

Db    979 GTGTGTGTGTGCTCAGCAGGAA 1000
```

```
RESULT  12
MUSNGF
LOCUS       MUSNGF       1176 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mouse nerve growth factor (NGF) precursor mRNA, complete cds.
ACCESSION   M35075 J00608
VERSION     M35075.1  GI:200047
KEYWORDS    nerve growth factor.
SOURCE      Mus musculus male submaxillary gland cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1176)
  AUTHORS   Scott,J., Selby,M., Urdea,M., Quiroga,M., Bell,G.I. and Rutter,W.J.
  TITLE     Isolation and nucleotide sequence of a cDNA encoding the precursor
            of mouse nerve growth factor
  JOURNAL   Nature 302, 538-540 (1983)
  MEDLINE   83167518
REFERENCE   2  (bases 3 to 226)
  AUTHORS   Edwards,R.H., Selby,M.J. and Rutter,W.J.
  TITLE     Differential RNA splicing predicts two distinct nerve growth factor
            precursors
  JOURNAL   Nature 319, 784-787 (1986)
  MEDLINE   86146860
FEATURES             Location/Qualifiers
     source          1. .1176
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /dev_stage="male"
                     /tissue_type="submaxillary gland"
     mRNA            1. .1176
                     /gene="NGF"
     gene            1. .1176
                     /gene="NGF"
     sig_peptide     96. .656
                     /gene="NGF"
     CDS             96. .1019
                     /partial
                     /gene="NGF"
                     /codon_start=1
                     /product="nerve growth factor"
                     /protein_id="AAA39818.1"
                     /db_xref="GI:387494"
                     /translation="MLCLKPVKLGSLEVGHGQHGGVLACGRAVQGAGWHAGPKLTSVS
                     GPNKGFAKDAAFYTGRSEVHSVMSMLFYTLITAFLIGVQAEPYTDSNVPEGDSVPEAH
                     WTKLQHSLDTALRRARSAPTAPIAARVTGQTRNITVDPRLFKKRRLHSPRVLFSTQPP
                     PTSSDTLDLDFQAHGTIPFNRTHRSKRSSTHPVFHMGEFSVCDSVSVWVGDKTTATDI
                     KGKEVTVLAEVNINNSVFRQYFFETKCRASNPVESGCRGIDSKHWNSYCTTTHTFVKA
                     LTTDEKQAAWRFIRIDTACVCVLSRKATRRG"
     mat_peptide     657. .1010
                     /gene="NGF"
                     /product="nerve growth factor"
BASE COUNT      283 a    330 c    295 g    268 t
ORIGIN
```

```
  Query Match           25.0%;  Score 99.6;  DB 12;  Length 1176;
  Best Local Similarity  58.4%;  Pred. No. 1.1e-15;
  Matches  223;  Conservative    0;  Mismatches  114;  Indels   45;  Gaps    1;

Qy      5 ccaacgacttcttgcatcgcggcgagtactctgtgtgtgacagcgaagagcactgggttg 64

Db    664 CCCACCCAGTCTTCCACATGGGGGAGTTCTCAGTGTGTGACAGTGTCAGTGTGTGGGTTG 723

Qy     65 gcaacctgacccaagccacagacttacggggcaatgaagtcacggtgctgccacatgttc 124

Db    724 GAGATAAGACCACAGCCACAGACATCAAGGGCAAGGAGGTGACAGTGCTGGCCGAGGTGA 783

Qy    125 gcatcaacaacgtggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcgaagc 184

Db    784 ACATTAACAACAGTGTATTCAGACAGTACTTTTTTGAGACCAAGTGCCGAGCCTCCAATC 843

Qy    185 ccatcggggcccccaagccgggtcaaggagtcagcggcgttaaagcaggaacctctagct 244

Db    844 CTGTTGAGAG----------------------------------------------TGGGT 858

Qy    245 gtcgtgggatcgacaacgagcactggaactcttattgcaccaacgtgcacacctttgtgc 304

Db    859 GCCGGGGCATCGACTCCAAACACTGGAACTCATACTGCACCACGACTCACACCTTCGTCA 918

Qy    305 gggcgttaacgtcctacaaaaaccagattgcctggaggttcatccgaatcaacgccgctt 364

Db    919 AGGCGTTGACAACAGATGAGAAGCAGGCTGCCTGGAGGTTCATCCGGATAGACACAGCCT 978

Qy    365 gcgtgtgcgtcctcagccgcaa 386

Db    979 GTGTGTGTGTGCTCAGCAGGAA 1000
```

```
RESULT  13
BOVNGFA
LOCUS       BOVNGFA       378 bp    mRNA            MAM       27-APR-1993
DEFINITION  Bovine nerve growth factor (NGF) mRNA, 3' end.
ACCESSION   M26809
VERSION     M26809.1  GI:163419
KEYWORDS    .
SOURCE      Bovine, cDNA to mRNA.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 378)
  AUTHORS   Meier,R., Becker-Andre,M., Goetz,R., Heumann,R., Shaw,A. and
            Thoenen,H.
  TITLE     Molecular cloning of bovine and chick nerve growth factor (NGF):
            Delineation of conserved and unconserved domains and their
            relationship to the biological activity and antigenicity of NGF
  JOURNAL   EMBO J. 5, 1489-1493 (1986)
  MEDLINE   86300647
FEATURES             Location/Qualifiers
     source          1. .378
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
     gene            1. .378
                     /gene="nerve growth factor"
     CDS             <1. .378
                     /gene="nerve growth factor"
                     /codon_start=1
                     /protein_id="AAA30666.1"
                     /db_xref="GI:163420"
```

```
                     /translation="HRSKRSSSHPVFHRGEFSVCDSISVWVGDKTTATDIKGKEVMVL
                     GEVNINNSVFKQYFFETKCRDPNPVDSGCRGIDAKHWNSYCTTTHTFVKALTMDGKQA
                     AWRFIRIDTACVCVLSRKTGQRA"
BASE COUNT       88 a    105 c    122 g     63 t
ORIGIN
```

```
  Query Match             24.6%;  Score 98;  DB 3;  Length 378;
  Best Local Similarity   58.1%;  Pred. No. 3.4e-15;
  Matches  222;  Conservative    0;  Mismatches  115;  Indels   45;  Gaps    1;

Qy       5 ccaacgacttcttgcatcgcggcgagtactctgtgtgtgacagcgaagagcactgggttg 64
           || ||  | |||| || || || |||| ||| ||||| ||||||          ||||||| 
Db      23 CCCACCCCGTCTTTCACCGGGGGGAGTTCTCGGTGTGCGACAGCATCAGCGTGTGGGTTG 82

Qy      65 gcaacctgacccaagccacagactt-acggggcaatgaagtcacggtgctgccacatgttc 124
           |  ||  |||    ||||| ||| |   |||||| || || | |||||||  | | ||
Db      83 GGGACAAGACAACGGCCACGGACATCAAGGGCAAGGAGGTGATGGTGCTGGGAGAGGTGA 142

Qy     125 gcatcaacaacgtggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcgaagc 184
           ||||||||||   ||    || |||   || |  ||||||| |||||| |   | || |
Db     143 ACATCAACAACAGTGTATTCAAACAGTACTTTTTTGAGACCAAGTGCCGGGACCCCAACC 202

Qy     185 ccatcggggcccccaagccgggtcaaggagtcagcggcgttaaagcaggaacctctagct 244
           || | |   |                                                | |
Db     203 CCGTGGACAGCG-----------------------------------------------GGT 217

Qy     245 gtcgtgggatcgacaacgagcactggaactcttattgcaccaacgtgcacacctttgtgc 304
           | || || ||||||    |||||||||| || ||||||||||     |||||||| ||
Db     218 GCCGAGGCATCGACGCGAAGCACTGGAATTCGTATTGCACCACGACCCACACCTTCGTCA 277

Qy     305 gggcgttaacgtcctacaaaaaccagattgcctggaggttcatccgaatcaacgccgctt 364
           |||| | ||     ||   || |||   |||||| |||||||||| ||| || | || |
Db     278 AGGCGCTGACCATGGACGGCAAGCAGGCCGCCTGGCGGTTCATCCGGATCGACACGGCCT 337

Qy     365 gcgtgtgcgtcctcagccgcaa 386
           ||||||| || |||||| | ||
Db     338 GCGTGTGTGTGCTCAGCAGGAA 359
```

```
RESULT  14
MUSNGFB
LOCUS       MUSNGFB      1164 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mouse beta-nerve growth factor (beta-NGF) mRNA.
ACCESSION   K01759
VERSION     K01759.1  GI:200051
KEYWORDS    nerve growth factor.
SOURCE      Mouse (male) submaxillary gland, cDNA to mRNA, clone pm-beta-N-9G1.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1164)
  AUTHORS   Ullrich,A., Gray,A., Berman,C.H. and Dull,T.J.
  TITLE     Human beta-nerve growth factor gene sequence highly homologous to
            that of mouse
  JOURNAL   Nature 303, 821-825 (1983)
  MEDLINE   83244969
COMMENT     Data kindly reviewed (18-OCT-1983) by A. Ullrich
            [1] identifies three possible translation initiation codons at
            bases 75-77, 273-275, and 279-281. They favor the second as the
            initiation site because the 16 amino acids that follow make a good
            candiate for a hydrophobic signal peptide and follows Kozak's rule.
            The exons are identified by homology studies with the human
            beta-NGF gene (see separate entry).
FEATURES             Location/Qualifiers
     source          1. .1164
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
     mRNA            <1. .>1164
                     /note="pbNGF mRNA"
     CDS             join(75. .136,137. .260,261. .998)
                     /partial
                     /note="prepro-beta-nerve growth factor"
                     /codon_start=1
                     /protein_id="AAA39820.1"
                     /db_xref="GI:387495"
                     /translation="MLCLKPVKLGSLEVGHGQHGGVLACGRAVQGAGWHAGPKLTSVS
                     GPNKGFAKDAAFYTGRSEVHSVMSMLFYTLITAFLIGVQAEPYTDSNVPEGDSVPEAH
                     WTKLQHSLDTALRRARSAPTAPIAARVTGQTRNITVDPRLFKKRRLHSPRVLFSTQPP
                     PTSSDTLDLDFQAHGTIPFNRTHRSKRSSTHPVFHMGEFSVCDSVSVWVGDKTTATDI
                     KGKEVTVLAEVNINNSVFRQYFFETKCRASNPVESGCRGIDSKHWNSYCTTTHTFVKA
                     LTTDEKQAAWRFIRIDTACVCVLSRKATRRG"
     exon            <75. .136
                     /note="prepro-beta-nerve growth factor"
                     /number=1
     exon            137. .260
     exon            261. .>998
                     /note="prepro-beta-nerve growth factor"
                     /number=3
     mat_peptide     636. .989
                     /note="beta-nerve growth factor"
BASE COUNT      284 a    327 c    284 g    269 t
ORIGIN      22 bp upstream of AluI site.
```

```
  Query Match             24.6%;  Score 98;  DB 12;  Length 1164;
  Best Local Similarity   58.1%;  Pred. No. 2.9e-15;
  Matches  222;  Conservative    0;  Mismatches  115;  Indels   45;  Gaps    1;

Qy       5 ccaacgacttcttgcatcgcggcgagtactctgtgtgtgacagcgaagagcactgggttg 64
           || ||     |||| ||    || |||| ||| ||||||||||| |        ||||||| 
Db     643 CCCACCCAGTCTTCCACATGGGGGAGTTCTCAGTGTGTGACAGTGTCAGTGTGTGGGTTG 702

Qy      65 gcaacctgacccaagccacagacttacggggcaatgaagtcacggtgctgccacatgttc 124
           |  |   ||||  |||||||||| |   |||||| || || || |||||| |  | ||
Db     703 GAGATAAGACCACAGCCACAGACATCAAGGGCAAGGAGGTGACAGTGCTGGCCGAGGTGA 762

Qy     125 gcatcaacaacgtggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcgaagc 184
           |||| ||||||   ||    |  |||   || |  |||||||| ||||||  |  || || |
Db     763 ACATTAACAACAGTGTATTCAGACAGTACTTTTTTGAGACCAAGTGCCGAGCCTCCAATC 822

Qy     185 ccatcggggcccccaagccgggtcaaggagtcagcggcgttaaagcaggaacctctagct 244
           |  | | |                                                | | |
Db     823 CTGTTGAGAG----------------------------------------------TGGGT 837

Qy     245 gtcgtgggatcgacaacgagcactggaactcttattgcaccaacgtgcacacctttgtgc 304
           | || || ||||||  | | ||||||||||| || |||||||     |||||||| ||
Db     838 GCCGGGGCATCGACTCCAAACACTGGAACTCATACTGCACCACGACTCACACCTTCGTCA 897

Qy     305 gggcgttaacgtcctacaaaaaccagattgcctggaggttcatccgaatcaacgccgctt 364
           |||||| ||  |  |  | || |||  ||| ||||||||||||| ||  || | || |
Db     898 AGGCGTTGACAACAGATGAGAAGCAGGCTGCTTGGAGGTTCATCCGGATAGACACAGCCT 957

Qy     365 gcgtgtgcgtcctcagccgcaa 386
           | ||||| || |||||| | ||
Db     958 GTGTGTGTGTGCTCAGCAGGAA 979
```

```
RESULT  15
MUSNGFBA
LOCUS       MUSNGFBA     1164 bp    mRNA            ROD       27-APR-1993
DEFINITION  Mouse nerve growth factor beta (beta-NGF) mRNA, complete cds.
ACCESSION   M14805
VERSION     M14805.1  GI:200053
KEYWORDS    nerve growth factor.
SOURCE      Mus musculus nerve cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1164)
  AUTHORS   Ullrich,A., Gray,A., Berman,C.H., Coussens,L. and Dull,T.J.
  TITLE     Sequence homology of human and mouse beta-NGF subunit genes
  JOURNAL   Cold Spring Harb. Symp. Quant. Biol. 48, 435-442 (1983)
  MEDLINE   84206565
FEATURES             Location/Qualifiers
     source          1. .1164
```

```
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /tissue_type="nerve"
     gene            75. .998
                     /gene="beta-NGF"
     CDS             75. .998
                     /gene="beta-NGF"
                     /codon_start=1
                     /product="nerve growth factor beta"
                     /protein_id="AAA39821.1"
                     /db_xref="GI:200054"
                     /translation="MLCLKPVKLGSLEVGHGQHGGVLACGRAVQGAGWHAGPKLTSVS
                     GPNKGFAKDAAFYTGRSEVHSVMSMLFYTLITAFLIGVQAEPYTDSNVPEGDSVPEAH
                     WTKLQHSLDTALRRARSAPTAPIAARVTGQTRNITVDPRLFKKRRLHSPRVLFSTQPP
                     PTSSDTLDLDFQAHGTIPFNRTHRSKRSSTHPVFHMGEFSVCDSVSVWVGDKTTATDI
                     KGKEVTVLAEVNINNSVFRQYFFETKCRASNPVESGCRGIDSKHWNSYCTTTHTFVKA
                     LTTDEKQAAWRFIRIDTACVCVLSRKATRRG"
BASE COUNT       284 a    327 c    284 g    269 t
ORIGIN
```

[redacted]uery Match 24.6%; Score 98; DB 12; Length 1164;
Best Local Similarity 58.1%; Pred. No. 2.9e-15;
Matches 222; Conservative 0; Mismatches 115; Indels 45; Gaps 1;

```
Qy       5 ccaacgacttcttgcatcgcggcgagtactctgtgtgtgacagcgaagagcactgggttg 64
Db     643 CCCACCCAGTCTTCCACATGGGGGAGTTCTCAGTGTGTGACAGTGTCAGTGTGTGGGTTG 702

Qy      65 gcaacctgacccaagccacagacttacggggcaatgaagtcacggtgctgccacatgttc 124
Db     703 GAGATAAGACCACAGCCACAGACATCAAGGGCAAGGAGGTGACAGTGCTGGCCGAGGTGA 762

Qy     125 gcatcaacaacgtggtgaagaagcagatgttctacgagaccacgtgccgtgtgtcgaagc 184
Db     763 ACATTAACAACAGTGTATTCAGACAGTACTTTTTTGAGACCAAGTGCCGAGCCTCCAATC 822

Qy     185 ccatcggggcccccaagccgggtcaaggagtcagcggcgttaaagcaggaacctctagct 244
Db     823 CTGTTGAGAG----------------------------------------------TGGGT 837

Qy     245 gtcgtgggatcgacaacgagcactggaactcttattgcaccaacgtgcacacctttgtgc 304
Db     838 GCCGGGGCATCGACTCCAAACACTGGAACTCATACTGCACCACGACTCACACCTTCGTCA 897

Qy     305 gggcgttaacgtcctacaaaaaccagattgcctggaggttcatccgaatcaacgccgctt 364
Db     898 AGGCGTTGACAACAGATGAGAAGCAGGCTGCTTGGAGGTTCATCCGGATAGACACAGCCT 957

[redacted]  365 gcgtgtgcgtcctcagccgcaa 386
Db     958 GTGTGTGTGTGCTCAGCAGGAA 979
```

Search completed: October 28, 2000, 20:46:24
Job time: 7165 sec